

PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/018,924

DATE: 01/17/2002
TIME: 07:15:17

Input Set : A:\SO042PCTSEQ.txt
Output Set: N:\CRF3\01172002\J018924.raw

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2 <110> APPLICANT: Shionogi & Co., Ltd
 4 <120> TITLE OF INVENTION: Composition for promoting passive extension of bladder smooth muscle
 W--> 5 <130> FILE REFERENCE: SO042PCT
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/018,924
 C--> 8 <141> CURRENT FILING DATE: 2001-12-19
 9 <150> PRIOR APPLICATION NUMBER: JP P1999-177549
 10 <151> PRIOR FILING DATE: 1999-06-23
 12 <160> NUMBER OF SEQ ID NOS: 6
 14 <170> SOFTWARE: PatentIn Ver. 2.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1457
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
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 23 <222> LOCATION: (165)..(719)
 25 <220> FEATURE:
 W-> 26 <221> NAME/KEY: mat peptide
 27 <222> LOCATION: (447)..(602)
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 32 ctggacttc ggagtttgc cattgccagt gggacgtctg agactttctc cttcaagtac 120
 34 ttggcagatc actctcttag cagggtctgc gtttcgcagc cggg atg aag ctg gtt 176
 35 Met Lys Leu Val
 37 tcc gtc gcc ctg atg tac ctg ggt tcg ctc gcc ttc cta ggc gct gac 224
 38 Ser Val Ala Leu Met Tyr Leu Gly Ser Leu Ala Phe Leu Gly Ala Asp
 39 -90 -85 -80 -75
 41 acc gct cgg ttg gat gtc gcg tcg gag ttt cga aag aag tgg aat aag 272
 42 Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys Lys Trp Asn Lys
 43 -70 -65 -60
 45 tgg gct ctg agt cgt ggg aag agg gaa ctg cgg atg tcc agc agc tac 320
 46 Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met Ser Ser Ser Tyr
 47 -55 -50 -45
 49 ccc acc ggg ctc gct gac gtg aag gcc ggg cct gcc cag acc ctt att 368
 50 Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala Gln Thr Leu Ile
 51 -40 -35 -30
 53 cgg ccc cag gac atg aag ggt gcc tct cga agc ccc gaa gac agc agt 416
 54 Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro Glu Asp Ser Ser
 55 -25 -20 -15
 57 ccg gat gcc gcc cgc atc cga gtc aag cgc tac cgc cag agc atg aac 464
 58 Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn
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 61 aac ttc cag ggc ctc cgg agc ttt ggc tgc cgc ttc ggg acg tgc acg 512
 62 Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe Gly Thr Cys Thr
 63 10 15 20
 65 gtg cag aag ctg gca cac cag atc tac cag ttc aca gat aag gac aag 560
 66 Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys

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70	Asp Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln Gly Tyr Gly Arg			
71	40	45	50	
73	cgg cgc cgg cgc tcc ctg ccc gag gcc ggc ccg ggt cgg act ctg gtg			656
74	Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly Arg Thr Leu Val			
75	55	60	65	70
77	tct tct aag cca caa gca cac ggg gct cca gcc ccc ccg agt gga agt			704
78	Ser Ser Lys Pro Gln Ala His Gly Ala Pro Ala Pro Pro Ser Gly Ser			
79	75	80	85	
81	gct ccc cac ttt ctt taggatttag gcgccatgg tacaaggaat agtcgcgcaa			759
82	Ala Pro His Phe Leu			
83	90			
85	gcatccccgt ggtgcctccc gggacgaagg acttcccgag cggtgtggg accgggctct			819
87	gacagccctg cggagaccct gagtccggga ggcacgcgtcc ggccggcgagc tctggctttg			879
89	caagggcccc tccttctggg ggcttcgtctt ccttagcctt gtcagggtgc aagtgcggcca			939
91	gggggggggg tgcaagaagaa tccgagtggt tgccagggtt aaggagagga gaaactgaga			999
93	aatgaatgtctg gagacccccc gggcgggggt ctgaggccaca gccgtgctcg cccacaaact			1059
95	gatttctcac ggcgtgtcac cccaccaggcg cgcaagcctc actattactt gaaccttcca			1119
97	aaacctaag aggaaaagtg caatgcgtgt tgtacataca gaggttaacta tcaatattta			1179
99	agtttgggtgc tgtcaagatt tttttgtaa cttcaaatat agagatatt ttgtacgtta			1239
101	tatattgtat taagggcatt taaaagcaa ttatattgtc ctccccattt ttaagacgtg			1299
103	aatgtctcag cgagggttaa agtttgcgc cgcgtggaat gtgagtggt gtgtgtgcatt			1359
105	gaaagagaaa gactgattac ctccgtgtc gaagaaggaa acaccgagtc tctgtataat			1419
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112	<212> TYPE: PRT			
113	<213> ORGANISM: Homo sapiens			
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119	Leu Gly Ala Asp Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys			
120	-75	-70	-65	
122	Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met			
123	-60	-55	-50	
125	Ser Ser Ser Tyr Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala			
126	-45	-40	-35	
128	Gln Thr Leu Ile Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro			
129	-30	-25	-20	-15
131	Glu Asp Ser Ser Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg			
132	-10	-5	-1	1
134	Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe			
135	5	10	15	
137	Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr			
138	20	25	30	
140	Asp Lys Asp Lys Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln			
141	35	40	45	50
143	Gly Tyr Gly Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly			

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160 <222> LOCATION: (148)..(711)			
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164 <222> LOCATION: (430)..(585)			
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169 tgccactgcc agaggacgt ctcagacttc atctcccaa atcttgcag atcacccct 120			
171 tagcagggtc tgcacatctc agccggg atg aag ctg gtt ccc gta gcc ctc atg 174			
172 Met Lys Leu Val Pro Val Ala Leu Met			
173	-90		
175 tac ctg ggc tcg ctc gcc ttc ctg ggc gct gac aca gct cgg ctc gac 222			
176 Tyr Leu Gly Ser Leu Ala Phe Leu Gly Ala Asp Thr Ala Arg Leu Asp			
177 -85	-80	-75	-70
179 gtg gcg gca gag ttc cga aag aaa tgg aat aag tgg gct cta agt cgt 270			
180 Val Ala Ala Glu Phe Arg Lys Lys Trp Asn Lys Trp Ala Leu Ser Arg			
181 -65	-60	-55	
183 gga aaa aga gaa ctt cgg ctg tcc agc agc tac ccc acc ggg atc gcc 318			
184 Gly Lys Arg Glu Leu Arg Leu Ser Ser Tyr Pro Thr Gly Ile Ala			
185 -50	-45	-40	
187 gac ttg aag gcc ggg cct gcc cag act gtc att cgg ccc cag gat gtg 366			
188 Asp Leu Lys Ala Gly Pro Ala Gln Thr Val Ile Arg Pro Gln Asp Val			
189 -35	-30	-25	
191 aag ggc tcc tct cgc agc ccc cag gcc agc att ccg gat gca gcc cgc 414			
192 Lys Gly Ser Ser Arg Ser Pro Gln Ala Ser Ile Pro Asp Ala Ala Arg			
193 -20	-15	-10	
195 atc cga gtc aag cgc tac cgc cag agt atg aac aac ttc cag ggc ctg 462			
196 Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn Asn Phe Gln Gly Leu			
197 -5	-1 1	5	10
199 cgg agc ttc ggc tgt cgc ttt ggg acg tgc acc gtc cag aag ctg gcg 510			
200 Arg Ser Phe Gly Cys Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala			
201 15	20	25	
203 cac cag atc tac cag ttc acg gac aaa gac aag gac ggc gtc gcc ccc 558			
204 His Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys Asp Gly Val Ala Pro			
205 30	35	40	
207 cgg agc aag atc agc ccc cag ggc tac ggc cgc cgg cgc cga cgc tct 606			
208 Arg Ser Lys Ile Ser Pro Gln Gly Tyr Gly Arg Arg Arg Arg Ser			
209 45	50	55	
211 ctg ccc gaa gcc agc ctg ggc cgg act ctg agg tcc cag gag cca cag 654			

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212 Leu Pro Glu Ala Ser Leu Gly Arg Thr Leu Arg Ser Gln Glu Pro Gln
 213 60 65 70 75
 215 gcg cac ggg gcc ccg gcc tcc ccg gcg cat caa gtg ctc gcc act ctc 702
 216 Ala His Gly Ala Pro Ala Ser Pro Ala His Gln Val Leu Ala Thr Leu
 217 80 85 90
 219 ttt agg att taggcgccta ctgtggcagc agcgaacagt cgcgcatgca 751
 220 Phe Arg Ile
 222 tcatgccgc gcttcctggg gcggggggct tcccgagcc gagccccctca gcggctgggg 811
 224 cccgggcaga gacagcattt agagaccgag agtccggag gcacagacca gcggcgagcc 871
 226 ctgcatttc aggaacccgt cctgcttgg agcgtgttc tcttcggctt aatccagccc 931
 228 gggtccccgg gtgggggtgg agggtgccaga ggaatccaaa ggagtgtcat ctgccaggct 991
 230 cacggagagg agaaactgcg aagtaaatgc ttagaccccc agggcaagg gtctgagcca 1051
 232 ctgccgtgcc gcccacaaac tgatttctga agggaaataa ccccaacagg ggcgaaggct 1111
 234 cactattact tgaactttcc aaaacctaga gaggaaaagt gcaatgtatg ttgtatataa 1171
 236 agaggttaact atcaatattt aagtttggc ctgtcaagat tttttttgt aacttcaa 1231
 238 atagagatat ttttgtacgt tatatatattgt attaaggc ttttaaaaaca attgtattgt 1291
 240 tcccctcccc tctatttaa tatgtgaatg tctcagcgg gtgtaacatt gtttgctgcg 1351
 242 cgaatgtga gagtgtgtgt gtgtgtgtgc gtggaaagaga gtctggatgc ctctgggga 1411
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 259 -75 -70 -65
 261 Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Leu
 262 -60 -55 -50
 264 Ser Ser Ser Tyr Pro Thr Gly Ile Ala Asp Leu Lys Ala Gly Pro Ala
 265 -45 -40 -35
 267 Gln Thr Val Ile Arg Pro Gln Asp Val Lys Gly Ser Ser Arg Ser Pro
 268 -30 -25 -20 -15
 270 Gln Ala Ser Ile Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg
 271 -10 -5 -1 1
 273 Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe
 274 5 10 15
 276 Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr
 277 20 25 30
 279 Asp Lys Asp Lys Asp Gly Val Ala Pro Arg Ser Lys Ile Ser Pro Gln
 280 35 40 45 50
 282 Gly Tyr Gly Arg Arg Arg Arg Ser Leu Pro Glu Ala Ser Leu Gly
 283 55 60 65
 285 Arg Thr Leu Arg Ser Gln Glu Pro Gln Ala His Gly Ala Pro Ala Ser
 286 70 75 80
 288 Pro Ala His Gln Val Leu Ala Thr Leu Phe Arg Ile
 289 85 90

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Input Set : A:\S0042PCTSEQ.txt
Output Set: N:\CRF3\01172002\J018924.raw

292 <210> SEQ ID NO: 5
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 294 <212> TYPE: DNA
 295 <213> ORGANISM: Rattus norvegicus
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 299 <222> LOCATION: (154)..(708)
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 303 <222> LOCATION: (433)..(582)
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 308 gttttgcgg ctgtcagaag gacgtctcg actttctgct tcaagtgc tacaactcac 120
 310 ccttcagca gggatcgaa gcatcgctac aga atg aag ctg gtt tcc atc gcc 174
 311 Met Lys Leu Val Ser Ile Ala
 312 -90
 314 ctg atg tta ttg ggt tcg ctc gcc gtt ctc ggc gcg gac acc gca cg 222
 315 Leu Met Leu Leu Gly Ser Leu Ala Val Leu Gly Ala Asp Thr Ala Arg
 316 -85 -80 -75
 318 ctc gac act tcc tcg cag ttc cga aag aag tgg aat aag tgg gcg cta 270
 319 Leu Asp Thr Ser Ser Gln Phe Arg Lys Lys Trp Asn Lys Trp Ala Leu
 320 -70 -65 -60 -55
 322 agt cgt ggg aag agg gaa cta caa gcg tcc agc agc tac cct acg ggg 318
 323 Ser Arg Gly Lys Arg Glu Leu Gln Ala Ser Ser Ser Tyr Pro Thr Gly
 324 -50 -45 -40
 326 ctc gtt gat gag aag aca gtc ccg acc cag act ctt ggg ctc cag gac 366
 327 Leu Val Asp Glu Lys Thr Val Pro Thr Gln Thr Leu Gly Leu Gln Asp
 328 -35 -30 -25
 330 aag cag agc acg tct agc acc cca caa gcc agc act cag agc aca gcc 414
 331 Lys Gln Ser Thr Ser Thr Pro Gln Ala Ser Thr Gln Ser Thr Ala
 332 -20 -15 -10
 334 cac att cga gtc aaa cgc tac cgc cag agc atg aac cag ggg tcc cgc 462
 335 His Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn Gln Gly Ser Arg
 336 -5 -1 1 5 10
 338 agc act gga tgc cgc ttt ggg acc tgc aca atg cag aaa ctg gct cac 510
 339 Ser Thr Gly Cys Arg Phe Gly Thr Cys Thr Met Gln Lys Leu Ala His
 340 15 20 25
 342 cag atc tac cag ttt aca gac aaa gac aag gac ggc atg gcc ccc aga 558
 343 Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys Asp Gly Met Ala Pro Arg
 344 30 35 40
 346 aac aag atc agc cct caa ggc tat ggc cgc cgg cgc cgt tcc ctg 606
 347 Asn Lys Ile Ser Pro Gln Gly Tyr Gly Arg Arg Arg Arg Ser Leu
 348 45 50 55
 350 cca gag gtc ctc cga gcc cgg act gtg gag tcc tcc cag gag cag aca 654
 351 Pro Glu Val Leu Arg Ala Arg Thr Val Glu Ser Ser Gln Glu Gln Thr
 352 60 65 70
 354 cac tca gct cca gcc tcc ccg gcg cac caa gac atc tcc aga gtc tct 702
 355 His Ser Ala Pro Ala Ser Pro Ala His Gln Asp Ile Ser Arg Val Ser
 356 75 80 85 90

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L:7 M:270 C: Current Application Number differs, Replaced Application Number
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:163 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:302 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5